Abstract

The three dimentional quantitative structure activity relationship (3D-QSAR) models including CoMFA and CoMSIA and molecular docking were built to reveal the relationship between molecular properties and biological activities on some Indolinone derivativesof PLK4 inhibitors as novel anti-proliferative agents and also were further suggested compounds with anticancer properties.CoMFA and CoMSIA models were constructed based on the most common structural subsets.Internal and external validation was performed to evaluate robustness and predictive power of the models. The statistical parameters from the models demonstrate the superiority of CoMFA in prediction over CoMSIA models. Molecular docking studies were also employed to study the molecular mechanisms of inhibitors. To propose new active compounds, the resulting CoMFA contour maps were used. Finally, *in silico* ADMET studies was performed on new design compounds to compare the computed ADMET descriptor values with the accepted ranges.

Keywords: 3D-QSAR, PLK4 inhibitors, CoMFA, CoMSIA, molecular docking, ADMET.

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